



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure



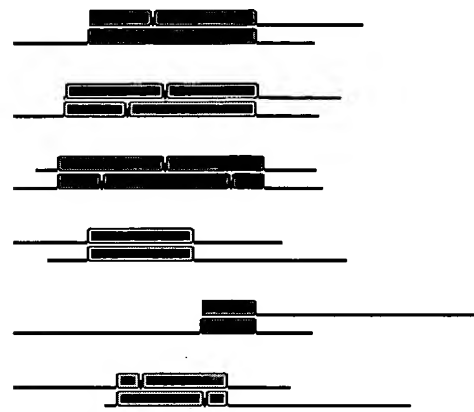
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

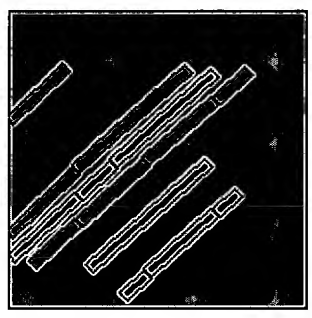
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Sequence 1 lcl|seq_1 Length 226 (1 .. 226) ——— Seq No 3
Sequence 2 lcl|seq_2 Length 250 (1 .. 250) ——— HS Rsp1

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2



1

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 77.8 bits (190), Expect = 7e-14
Identities = 47/138 (34%), Positives = 73/138 (52%), Gaps = 1/138 (0%)



Query: 1 MRILDLPKNQISHLP AEIGCLKNLKE LNVGFNYLKSIPPELGDCENLERLDCS-GNLELM 59
+ +L+ NQI LP +I L+ LK LN+G N L ++P G LE LD + NL
Sbjct: 65 LEVLNFFN NQIEELPTQISSLQKLKHLNLGMNRLNTLPRGFGSLPALEVL DLTYN NLS EN 124

Query: 60 ELPFELS NLKQVTFVDISANKFSSVPICVLRMSNLQWLDISSNNLT DLPQDIDRLEELQS 119
LP L + + +S N F +P + +++ LQ L + N+L LP++I L +L+
Sbjct: 125 SLPGNFFYLTTLRALYLS DNDFEILPPDIGKLT KLQILSLRDNDLISLPKEIGELTQLKE 184

Query: 120 FLLYKNKLTYLPYSMLNL 137
+ N+LT LP + NL
Sbjct: 185 LHIQGNRLTVLPPELGNL 202

Score = 67.8 bits (164), Expect = 7e-11
Identities = 49/156 (31%), Positives = 79/156 (50%), Gaps = 3/156 (1%)



Query: 4 LDLPKNQISHLP AEIGCLKNLKE LNVGFNYLKSIPPELGDCENLERLDCSGNLELMELPF 63
L L N+++ +P I LKNL+ LN N ++ +P ++ + L+ L+ N L LP
Sbjct: 45 LVLSHNKLTMVPPNIAELKNLEVLNFFN NQIEELPTQISSLQKLKHLNLGMN-RLNTLPR 103

Query: 64 ELSNLKQVTFVDISANKFS--SVPICVLRMSNLQWLDISSNNLT DLPQDIDRLEELQSFL 121

+L + +D++ N S S+P ++ L+ L +S N+ LP DI +L +LQ
 Sbjct: 104 GFGSLPALEVLDLTYNNSLSESLPGNFFYLTTLRALYLSDNDFEILPPDIGKLTQLQILS 163
 Query: 122 LYKNKLTYPYSMLNLKKLTLLVSGDHLVELPTAL 157
 L N L LP + L +L L + G+ L LP L
 Sbjct: 164 LRDNDLISLPKEIGELTQLKELHIQGNRLTVLPPEL 199

Score = 66.2 bits (160), Expect = 2e-10
 Identities = 46/165 (27%), Positives = 88/165 (52%), Gaps = 4/165 (2%)

Query: 21 LKNLKELNVGFNYLKSIPPELGDCENLERLDCSGNLELMELPFELSNLKQVTFVDISANK 80
 L ++ +L + N L +PP + + +NLE L+ N ++ ELP ++S+L+++ +++ N+
 Sbjct: 39 LSHITQLVLSHNKLTMVPPNIAELKNLEVLNFFNN-QIEELPTQISSLQKLKHLNLMNR 97
 Query: 81 FSSVPICVLRMSNLQWLDISSNNLTD--LPQDIDRLEELQSFLLYKNKLTYPYSMLNLK 138
 +++P + L+ LD++ NNL++ LP + L L++ L N LP + L
 Sbjct: 98 LNTLPRGFGSLPALEVLDLTYNNSLSESLPGNFFYLTTLRALYLSDNDFEILPPDIGKLT 157

Query: 139 KLTLVSGDHLVELPTALCDSSTPLKFVSLMDNPIDNAQCEDGN 183
 KL +L + + L+ LP + T LK + + N + E GN
 Sbjct: 158 KLQILSLRDNDLISLPKEI-GELTQLKELHIQGNRLTVLPPELGN 201

Score = 45.8 bits (107), Expect = 3e-04
 Identities = 27/88 (30%), Positives = 48/88 (53%)

Query: 65 LSNLKQVTFVDISANKFSSVPICVLRMSNLQWLDISSNNLTDLPQDIDRLEELQSFLLYK 124
 L L +T + +S NK + VP + + NL+ L+ +N + +LP I L++L+ L
 Sbjct: 36 LFTLSHITQLVLSHNKLTMVPPNIAELKNLEVLNFFNNQIEELPTQISSLQKLKHLNLM 95
 Query: 125 NKLTYPYSMLNLKKLTLLVSGDHLVE 152
 N+L LP +L L +L ++ ++L E
 Sbjct: 96 NRLNTLPRGFGSLPALEVLDLTYNNSLSE 123

Score = 41.6 bits (96), Expect = 0.005
 Identities = 21/45 (46%), Positives = 29/45 (63%)

Query: 1 MRILDLPKNQISHLPAEIGCLKNLKELNVGFNYLKSIPPELGDC 45
 ++IL L N + LP EIG L LKEL++ N L +PPELG+ +
 Sbjct: 159 LQILSLRDNDLISLPKEIGELTQLKELHIQGNRLTVLPPELGNLD 203

Score = 32.3 bits (72), Expect = 3.2
 Identities = 24/88 (27%), Positives = 44/88 (49%), Gaps = 3/88 (3%)

Query: 90 RMSNLQWLDISSNNLTDL--PQDIDRLEELQSFLLYKNKLTYPYSMLNLKKLTLLVSG 147
 R N +D+S +++ + L + +L NKLT +P ++ LK L +L
 Sbjct: 13 REKNQPEVDMSDRGISNMLDVNGFLTSLHITQLVLSHNKLTMVPPNIAELKNLEVLNFFN 72
 Query: 148 DHLVELPTALCDSSTPLKFVSLMDNPID 175
 + + ELPT + S LK ++L N ++
 Sbjct: 73 NQIEELPTQI-SSLQKLKHLNLMNRNLN 99

CPU time: 0.10 user secs. 0.04 sys. secs 0.14 total secs.

Lambda K H

0.317 0.136 0.387

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 757

Number of Sequences: 0

Number of extensions: 78

Number of successful extensions: 16

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 8

length of query: 226

length of database: 324,428,749

effective HSP length: 115

effective length of query: 111

effective length of database: 159,343,374

effective search space: 17687114514

effective search space used: 17687114514

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 68 (30.8 bits)